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ATGGCTTTGG	AACAGAACCA	GTCAACAGAT	TATTATTATG	AGGAAAATGA	50
M A L E	Q N Q	S T D	Y Y Y E	E N E	
AATGAATGGC	ACTTATGACT	ACAGTCAATA	TGAACTGATC	TGTATCAAAG	100
M N G	T Y D Y	S Q Y	E L I	C I K E	
AAGATGTCAG	AGAATTTGCA	AAAGTTTTCC	TCCCTGTATT	CCTCACAATA	150
D V R	E F A	K V F L	P V F	L T I	
GTTTTCGTCA	TTGGACTTGC	AGGCAATTCC	ATGGTAGTGG	CAATTTATGC	200
V F V I	G L A	G N S	M V V A	I Y A	
CTATTACAAG	AAACAGAGAA	CCAAAACAGA	TGTGTACATC	CTGAATTTGG	250
Y Y K	K Q R T	K T D	V Y I	L N L A	
CTGTAGCAGA	TTTACTCCTT	CTATTCACCTC	TGCCTTTTTG	GGCTGTTAAT	300
V A D	L L L	L F T L	P F W	A V N	
GCAGTTCATG	GGTGGGTTTT	AGGGAAAATA	ATGTGCAAAA	TAACTTCAGC	350
A V H G	W V L	G K I	M C K I	T S A	
CTTGATACACA	CTAAACTTTG	TCTCTGGAAT	GCAGTTTCTG	GCTTGTATCA	400
L Y T	L N F V	S G M	Q F L	A C I S	
GCATAGACAG	ATATGTGGCA	GTAATAAAG	TCCCCAGCCA	ATCAGGAGTG	450
I D R	Y V A	V T K V	P S Q	S G V	
GAAAACCAT	GCTGGATCAT	CTGTTTCTGT	GTCTGGATGG	CTGCCATCTT	500
G K P C	W I I	C F C	V W M A	A I L	
GCTGAGCATA	CCCCAGCTGG	TTTTTTATAC	AGTAAATGAC	AATGCTAGGT	550
L S I	P Q L V	F Y T	V N D	N A R C	
GCATTCCCAT	TTTCCCCCGC	TACCTAGGAA	CATCAATGAA	AGCATTGATT	600
I P I	F P R	Y L G T	S M K	A L I	
CAAATGCTAG	AGATCTGCAT	TGGATTTGTA	GTACCCTTTC	TTATTATGGG	650
Q M L E	I C I	G F V	V P F L	I M G	
GGTGTGCTAC	TTTATCACAG	CAAGGACACT	CATGAAGATG	CCAAACATTA	700
V C Y	F I T A	R T L	M K M	P N I K	
AAATATCTCG	ACCCCTAAAA	GTTCTGCTCA	CAGTCGTTAT	AGTTTTTCATT	750
I S R	P L K	V L L T	V V I	V F I	
GTCACTCAAC	TGCCTTATAA	CATTGTCAAG	TTCTGCCGAG	CCATAGACAT	800
V T Q L	P Y N	I V K	F C R A	I D I	
CATCTACTCC	CTGATCACCA	GCTGCAACAT	GAGCAAACGC	ATGGACATCG	850
I Y S	L I T S	C N M	S K R	M D I A	
CCATCCAAGT	CACAGAAAGC	ATCGCACTCT	TTACAGCTG	CCTCAACCCA	900
I Q V	T E S	I A L F	H S C	L N P	
ATCCTTTATG	TTTTTATGGG	AGCATCTTTC	AAAAACTACG	TTATGAAAGT	950
I L Y V	F M G	A S F	K N Y V	M K V	
GGCCAAGAAA	TATGGGTCCT	GGAGAAGACA	GAGACAAAGT	GTGGAGGAGT	1000
A K K	Y G S W	R R Q	R Q S	V E E F	
TTCCTTTTGA	TTCTGAGGGT	CCTACAGAGC	CAACCAGTAC	TTTTAGCATT	1050
P F D	S E G	P T E P	T S T	F S I	
TAAAGGTAAG	ACTGCTCTGC	CTTTTGCTTG	GATACATATG	AATGATGCTT	1100
- R - N	C S A	F C L	D T Y E	- C F	
TCCCCTCAAA	TAAAACATCT	GCCTTATTCT	GAAAAAAM	AAAAAAM	1147
P L K	- N I C	L I L	K K K	K K	

FIG. 1



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CCX-CKR MALEQNQSTDYYYE--ENEMNGTY-----DYSQYELIQIK 33
CCR9 MTPTDFTSPIPNMADDYG-SESTSSM-EDYVN----FNFTDF--YCEK
CCR7 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLQSK
CCR6 MSGESMNFSDVFDSSDYFVS-----VNTSMYS-----VDSEML--LQSL
STRL33 MAEHDYHEDYGFSGS-----SF-NDSSQEEHQDF--L---

TM1

CCX-CKR EDVREFAKVFLFVFLTIVFVIGTAGNSMVVAIMAYYKKQRTKTQDVYLLNL 83
CCR9 NNVRQEFASHFLFPLYWLVEIVGALGNSLMILVWYCTRVKMTDMFLLNL
CCR7 KDVRNFKAWFLFIMYSIICFVGILGNGLVVLTYYIFKRLKIMTDTYLLNL
CCR6 QEVRQFSRLFMFIAYSLICQVFGILGMLLVITFAFYKARSMTDQVYLLNM
STRL33 ----QESKVELECMYLVFVCGIVGNSLMVISIFMHLQSLTDVFLVNL

TM2

TM3

CCX-CKR AMADLLLLFTLPFWAV-NAVHGWVLCKIMCKITSALYTLNFMVSGMOFLAC 132
CCR9 AIADLLFLVTLFPWATA-AADQWKFOFMCKVNSMYKMFYSCVLLIMC
CCR7 AMADILFLLTLFPWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGMLLLC
CCR6 AIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIMAINFNCGMLLLTC
STRL33 PLADLVFVCTLPFWAYA-GIHEWVFGVMCKSLLGIYTFNYTSMILLTC

TM4

CCX-CKR ISIDRYVAVTK-VPSQSGVGKP---CWIICFCVMMAAILLSIEQLVFTV 178
CCR9 ISMDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWLAAALCIEILYSQI
CCR7 ISIDRYVAIVQAVSAHRHRARVLLISKLSGVGSAILATVLSIEHELLYSDL
CCR6 ISMDRYIAIVQATKSFLRSRTLPRTKIIQLVWGLSVIISSTFVFNQK
STRL33 ITVDHFIVVVKATKAYNQQAQRMTWGVKVTSLLIWISLLVSLFOIYGNV

TM5

CCX-CKR NDNAR---CIPIFPRY-LGTSMKALIQMLEICIGFVVPFLIMGVCFYITA 224
CCR9 KEESGIAICTMVYPS-DESTKLKSAVLTLLKVILGFFLEFVVMACCYTII
CCR7 QRSSEQAMRCSLIT-EHVEAF-ITIQVAMVIGFLVPLLAMSFCYLVII
CCR6 YNTQGSDVCEPKYQTVSEPIRWKLLMLGLLELLFGFFIPLMFMIFCYTFIV
STRL33 FNLDKL-IC--GYH--DEAIS--TVVLATQMTLGEFFLELLTMIVCYSVII

TM6

CCX-CKR RTLMKMPNIIKISRELKVLLTVIIVFIVTOLPYNIVKFCRAIDIIYSLITS 274
CCR9 HTLIQAKKSSKHKALKVTITVLTIVFVLSQFPYNCILLVQTIDAYAMFISN
CCR7 RTLLQARNFERNKAIKVIIAVVVFIVFOLPYNGVLAQTVANFNITSST
CCR6 KTLVQAQNSKRHKAIKRMIIAVVLVFLACQIPHNMVLLV-TAANLGKMNR
STRL33 KTLHAGGFQKHRSKLIIFLVMAVELLTOMPFNLMKFIRSTH-----WE

FIG. 2A

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TM7

CCX-CKR	CNMSKRMDDIAIQVTESTALFHISCLNEILYVFMGASFKNYVMK-----V 317
CCR9	CAVSTNIDICFQVTQTIAFFHISCLNEVLVVFVGERFRDLVKTLKNLGCI
CCR7	CELSKQLNTAYDVTYSLACVRCVNFFLYAFIGVKFRNDIFKLFKDLGCL
CCR6	COSEKLIGYTKIVTEVLAFHCLNEVLVAFIGQKFRNYFLKILKDLWCV
STRL33	YYAMTSFHYTIMVTEATAYLRACLNEVLVAFVSLKFRKNFWKLVKDIGCL

CCX-CKR	AKKY--GSWRRQRQSV--EFPFDSEGP--TEPTSTFSI	350
CCR9	SQA-QWVSFTR----REGSLK-LSSMLLETTSGALSL	
CCR7	SQE-QLRQWSS----CRHIRR-SSMSVEAETTTTFSP	
CCR6	RRKYKSSGFSCAGRYSENISRQTSETADNDNASSTFM	
STRL33	P--Y--LGVSHQWKSS--DNSKTF SASHNVEATSMFQL	

FIG. 2A
(CONTINUED)

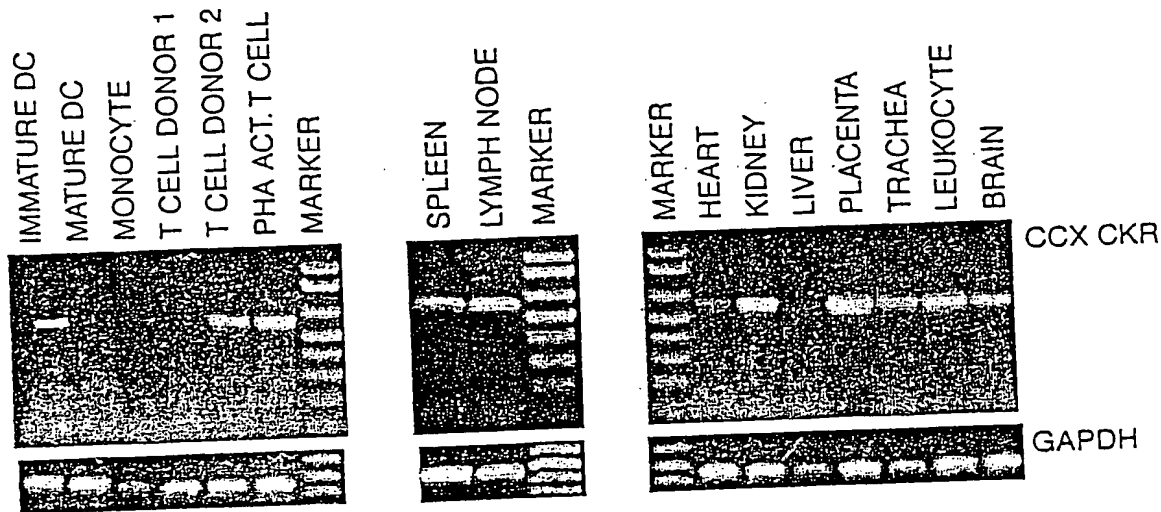


FIG. 2B

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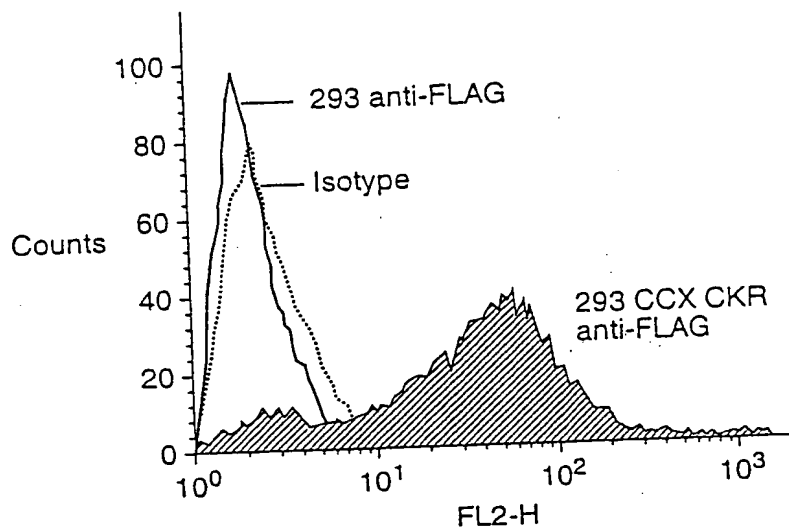


FIG. 2C

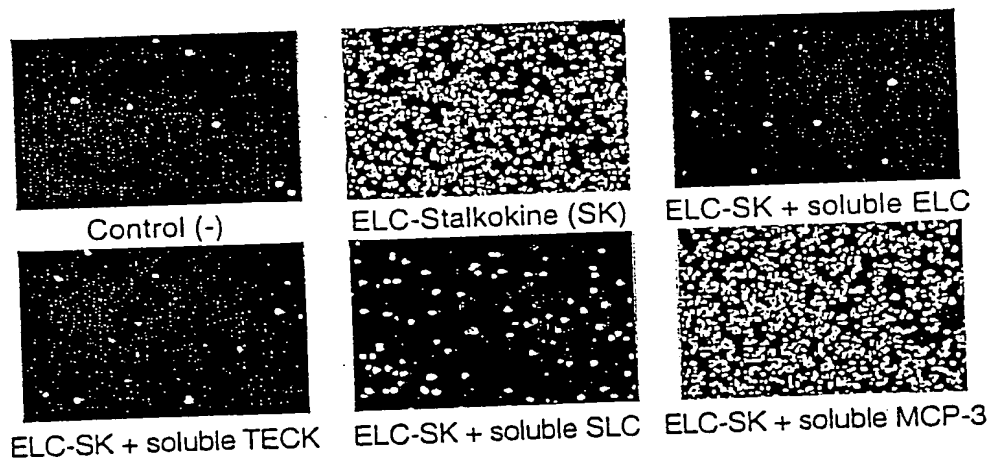


FIG. 3A

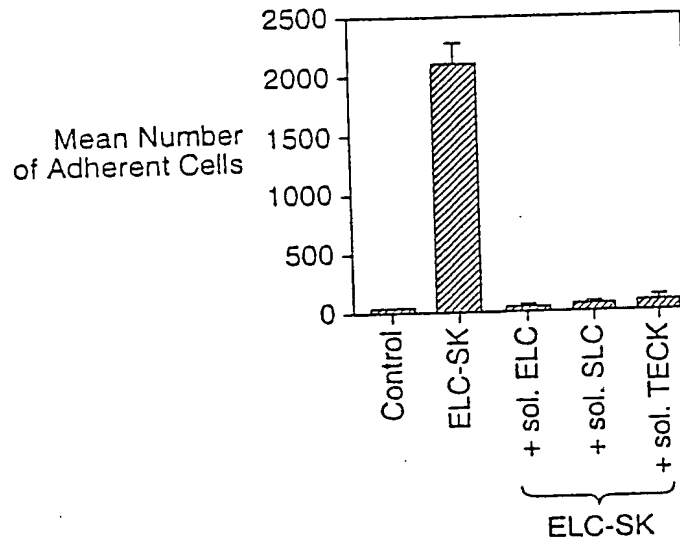


FIG. 3B

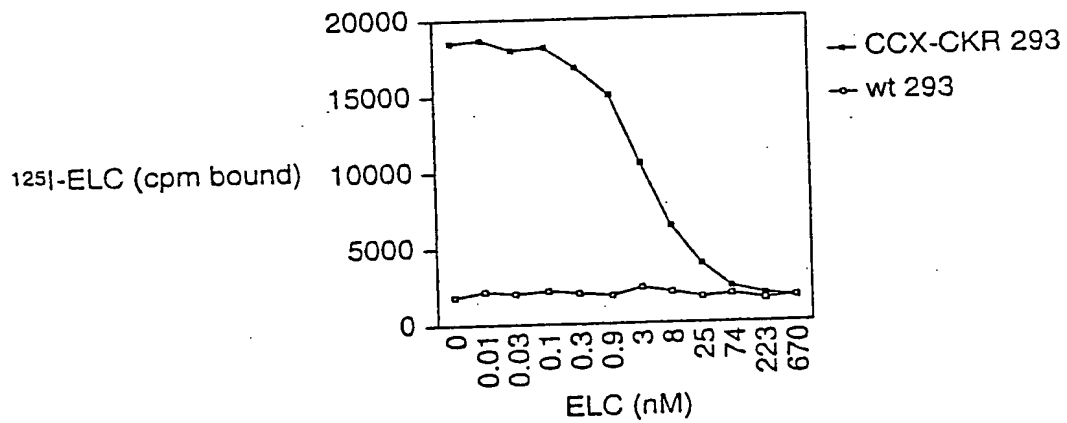


FIG. 3C

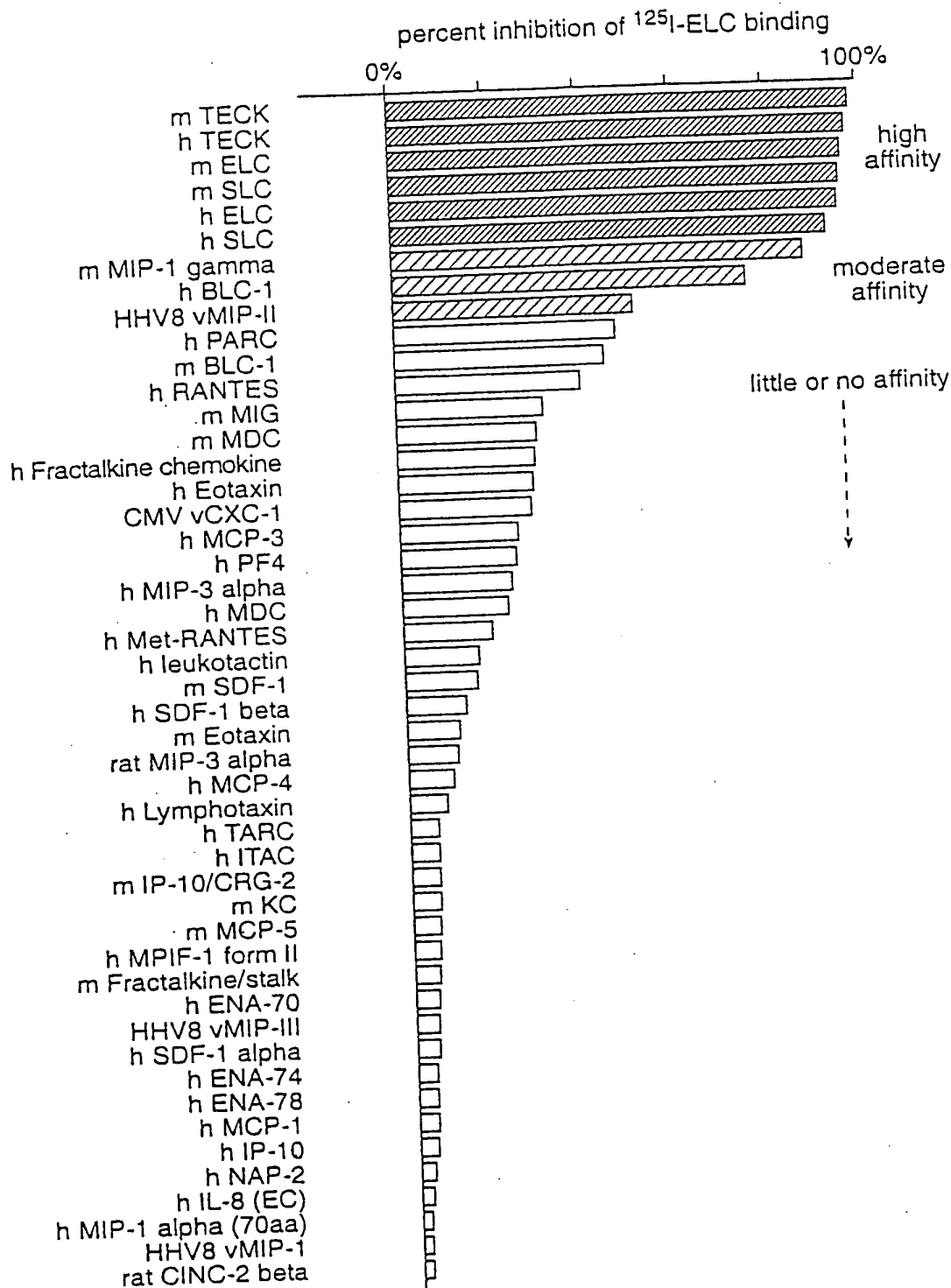


FIG. 4A



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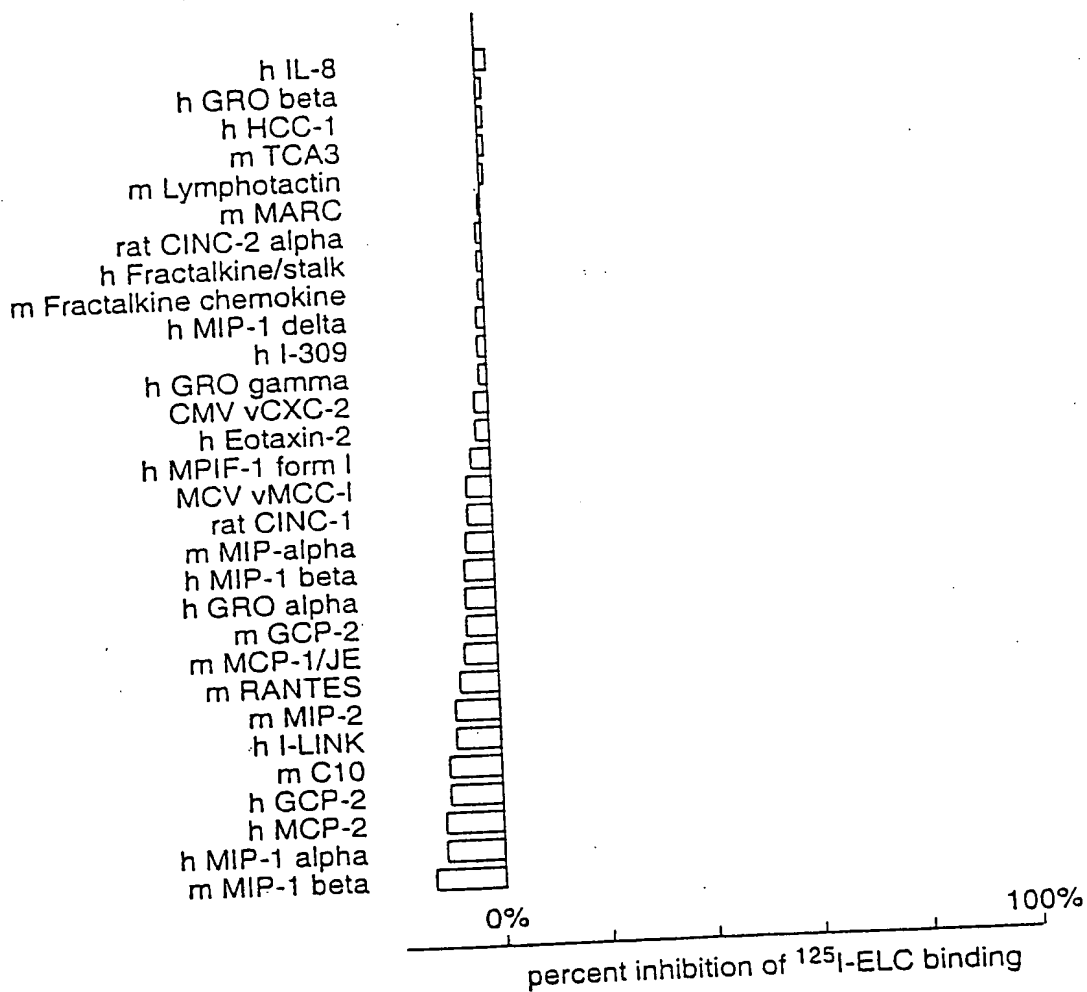
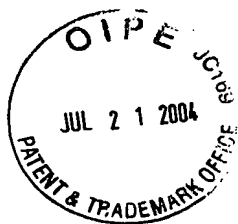
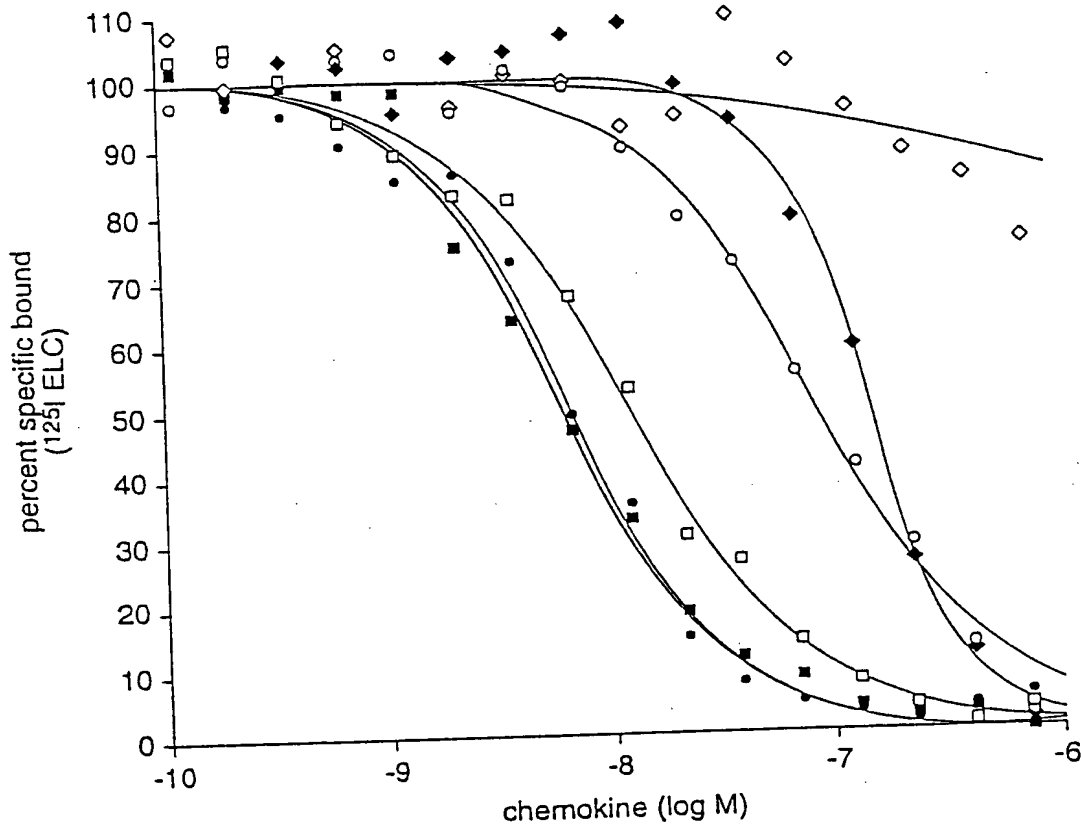


FIG. 4A
(CONTINUED)



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human chemokines		murine chemokines	
	IC-50		IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
• h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B



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5'upstream CCXCKR	ATGCAGCATC	TCGTTTATAA	AAGGCAACTA	GTGAAATTTA	GTGCAAATGC	50
5'upstream CCXCKR	TGAGAGAATT	TATTTAACTT	ATTTAAATTA	AATTTATAAA	TAACATCAAA	100
5'upstream CCXCKR	ATAAAAAATA	AATTTAATTT	AAATAAACCA	AGTAATTTGC	TATTTTCGTT	150
5'upstream CCXCKR	TTTATTCAAT	TTGTTGTAGA	TATACTTTTA	CGATTCACAA	AATTATGTAT	200
5'upstream CCXCKR	GTAAAGATTA	TAACACTATT	TATTCTTTTT	AGTTAAAATC	TAATTAAATT	250
5'upstream CCXCKR	TTCATATTTT	AAAAATCATT	TTTACATAAA	AGTCTTCACT	TTTATTTAGG	300
5'upstream CCXCKR	ATTTAATGAT	TAAGAAAATT	CTCCAGGGCA	TTATGTTTAT	TGTCCTGTTC	350
5'upstream CCXCKR	AAATCCAAGC	TCTTTCACAC	AGAATTGTAC	AAGCAAAGTT	TGAGTAACTA	400
5'upstream CCXCKR	ATCTTGGGGT	CATATTCCAA	TGTGGCTCCC	ATTAAAGCAT	TTCAAAGAGT	450
5'upstream CCXCKR	GCTAGATTCA	GGCTCACATA	TGTTACAGCA	ACAGGCTATA	CTCTAGGGAA	500
5'upstream CCXCKR	AGAACAAAAC	AGCTTGATAG	AAACTGTGTG	CTTTAAGCA	TATTTAGACA	550
5'upstream CCXCKR	AATATCTATC	CTGTATTCTC	TTTGCCATCT	AGATTGGAGC	CATGGCTTTG	600
					ATGGCTTTG	9
5'upstream CCXCKR	GAACAGAACC	GTCAACAGA	TTATTATTAT	GAGGAGAGT	GAAATGAATG	649
	GAACAGAACC	AGTCAACAGA	TTATTATTAT	GAGGA-AAA	GAAATGAATG	58
5'upstream CCXCKR	GC-CTGATGA	CTACAGTCAG	TATGAACTGA	TCTGT-----	TC	685.
	GCACTTATGA	CTACAGTCFA	TATGAACTGA	TCTGTATCAA	AGAAGATGTC	108
5'upstream CCXCKR	AGAGAAAGAGA	CAGAGGATAT	GC-ACAGGGT	TGCTCCCTGT	ATTGCTCACC	734
	AGAGAA-----	TTT GCAAAAGTTT	TGCTCCCTGT	ATTGCTCACA		147
5'upstream CCXCKR	ATAG-----			AG-----		740
	ATAGTTTTCG	TCATTGGACT	TGCAGGCAAT	TCCATGGTAG	TGGCAATTTA	197
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
	TGCCTATTAC	AAGAAACAGA	GAACCAAAAC	AGATGTGTAC	ATCCTGAATT	247
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
	TGGCTGTAGC	AGATTTACTC	CTTCTATTCA	CTCTGCCTTT	TTGGGCTGTT	297
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
	AATGCAGTTC	ATGGGTGGGT	TTTAGGGAAA	ATAATGTGCA	AAATAACTTC	347

FIG. 5

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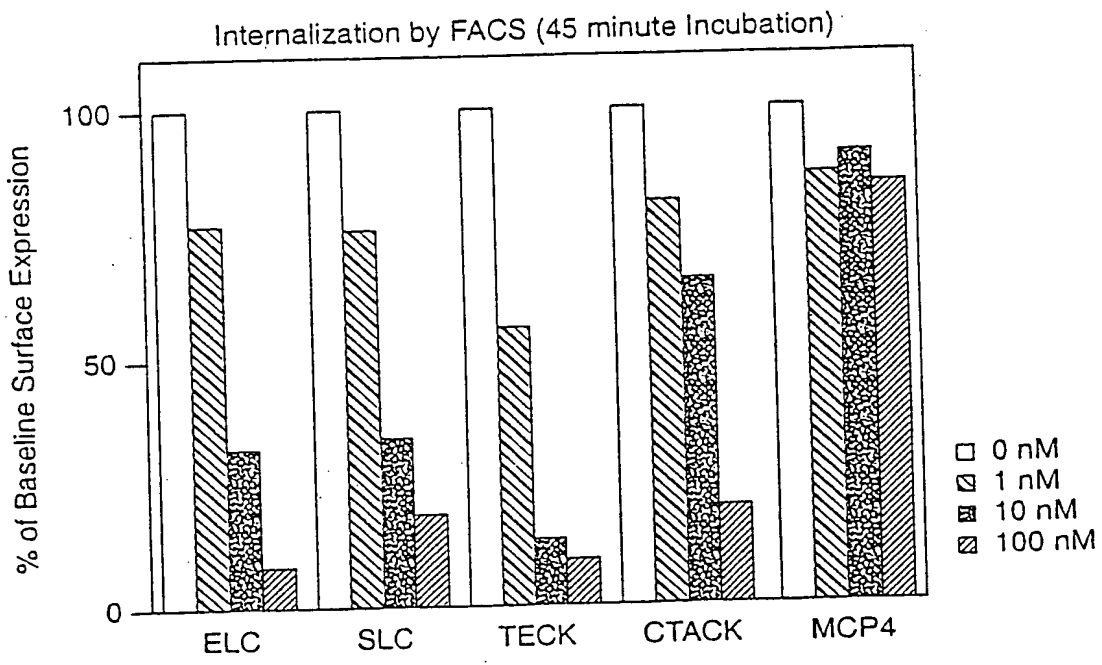


FIG. 6A

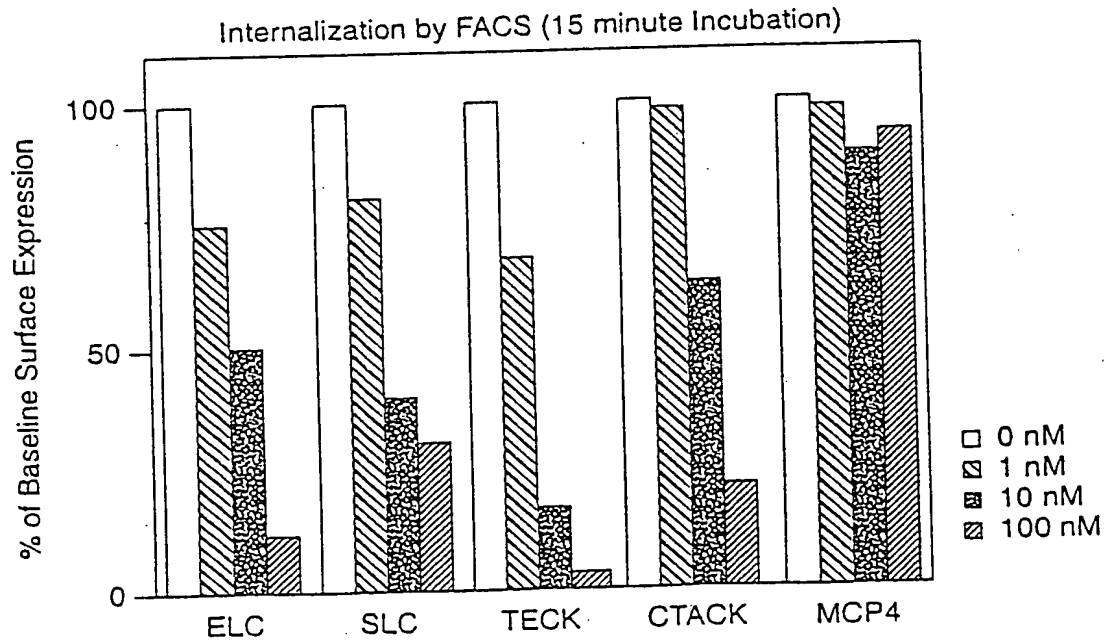


FIG. 6B